



BIZ-045CPCN

SEQUENCE LISTING

<110> Lu, Kung Ping
Wulf, Gerbung
Xiao, Zhen Zhou

<120> PIN1 as a Marker for Abnormal Cell Growth

<130> BIZ-045CPCN

<140> 10/683880

<141> 2003-10-09

<150> 09/726464

<151> 2000-11-29

<150> 60/167800

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<150> 60/253676

<151> 2000-11-28

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<170> FastSEQ for Windows Version 4.0

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<212> DNA

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| 1 | TGCTGGCCAG CACCTCGAGG GAAG ATG GCG GAC GAG GAG AAG CTG CCG CCC | 51 |
| | Met Ala Asp Glu Glu Lys Leu Pro Pro | |
| 10 | GGC TGG GAG AAG CGC ATG AGC CGC AGC TCA GGC CGA GTG TAC TAC TTC | 99 |
| | Gly Trp Glu Lys Arg Met Ser Arg Ser Ser Gly Arg Val Tyr Tyr Phe | |
| 15 | AAC CAC ATC ACT AAC GCC AGC CAG TGG GAG CGG CCC AGC GGC AAC AGC | 147 |
| | Asn His Ile Thr Asn Ala Ser Gln Trp Glu Arg Pro Ser Gly Asn Ser | |
| 30 | AGC AGT GGT GGC AAA AAC GGG CAG GGG GAG CCT GCC AGG GTC CGC TGC | 195 |
| | Ser Ser Gly Gly Lys Asn Gly Gln Gly Glu Pro Ala Arg Val Arg Cys | |
| 45 | TCG CAC CTG CTG GTG AAG CAC AGC CAG TCA CGG CGG CCC TCG TCC TGG | 243 |
| | Ser His Leu Leu Val Lys His Ser Gln Ser Arg Arg Pro Ser Ser Trp | |
| 60 | CGG CAG GAG AAG ATC ACC CGG ACC AAG GAG GAG GCC CTG GAG CTG ATC | 291 |
| | Arg Gln Glu Lys Ile Thr Arg Thr Lys Glu Glu Ala Leu Glu Leu Ile | |
| 75 | AAC GGC TAC ATC CAG AAG ATC AAG TCG GGA GAG GAG GAC TTT GAG TCT | 339 |
| | Asn Gly Tyr Ile Gln Lys Ile Lys Ser Gly Glu Glu Asp Phe Glu Ser | |
| 90 | CTG GCC TCA CAG TTC AGC GAC TGC AGC TCA GCC AAG GCC AGG GGA GAC | 387 |
| | Leu Ala Ser Gln Phe Ser Asp Cys Ser Ser Ala Lys Ala Arg Gly Asp | |
| 110 | | 115 |
| | | 120 |

CTG GGT GCC TTC AGC AGA GGT CAG ATG CAG AAG CCA TTT GAA GAC GCC 435
 Leu Gly Ala Phe Ser Arg Gly Gln Met Gln Lys Pro Phe Glu Asp Ala
 125 130 135

TCG TTT GCG CTG CGG ACG GGG GAG ATG AGC GGG CCC GTG TTC ACG GAT 483
 Ser Phe Ala Leu Arg Thr Gly Glu Met Ser Gly Pro Val Phe Thr Asp
 140 145 150

tcc ggc atc cac atc atc ctc cgc act gag tgaggggtggg gagcccaggc 533
 Ser Gly Ile His Ile Ile Leu Arg Thr Glu
 155 160

ctggcctcgg ggcagggcag ggcggctagg ccggccagct ccccttgcc cgccagccag 593

tggccgaacc cccactccc tgccaccgtc acacagtatt tattgttccc acaatggctg 653

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gggctgcgac cgccagattc tcccttaagg aattgacttc agcaggggtg ggaggctccc 773

agaccagggg cagtgtggtg ggaggggtgt tccaaagaga aggcctggtc agcagagccg 833

ccccgtgtcc cccaggtgc tggaggcaga ctcgagggcc gaattgtttc tagttaggcc 893

acgctcctct gttcagtcgc aaaggtgaac actcatgagg cagccatggg ccctctgagc 953

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 <212> PRT
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Gln Trp Glu Arg Pro Ser Gly Asn Ser Ser Ser Gly Gly Lys Asn Gly
 35 40 45

Gln Gly Glu Pro Ala Arg Val Arg Cys Ser His Leu Leu Val Lys His
 50 55 60

Ser Gln Ser Arg Arg Pro Ser Ser Trp Arg Gln Glu Lys Ile Thr Arg
 65 70 75 80

Thr Lys Glu Glu Ala Leu Glu Leu Ile Asn Gly Tyr Ile Gln Lys Ile
 85 90 95

Lys Ser Gly Glu Glu Asp Phe Glu Ser Leu Ala Ser Gln Phe Ser Asp
 100 105 110

Cys Ser Ser Ala Lys Ala Arg Gly Asp Leu Gly Ala Phe Ser Arg Gly
 115 120 125

Gln Met Gln Lys Pro Phe Glu Asp Ala Ser Phe Ala Leu Arg Thr Gly
 130 135 140

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Glu Met Ser Gly Pro Val Phe Thr Asp Ser Gly Ile His Ile Ile Leu
145 150 155 160

Arg Thr Glu